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FIG. 1

Exon-Intron Boundary Sequences of the Human alpha-7 nAChR Subunit Gene

Exon Number	Exon length (bp)	cDNA position	splice acceptor	flanking exon sequence	splice donor	Intron number	Intron Size approximate (Kb)
1	55	1-55		...CTG CAC G L H	GTAAAGCCAC	1	0.3
2	140	56-195	TCTCCTTAAG	TG TCC.....GAC GTG V S D V	GTGAGTCCCG	2	Unknown
3	45	196-240	TTTTTTGAAG	GAT GAG.....CAA ATG D E Q M	GTAAGTTAAG	3	9.0
4	110	241-350	TGTGTGTCAG	TCT TGG.....AAC AG S W N S	GTAAGCATAT	4	Unknown
5	80	351-430	CTGTTTCTAG T	GCT GAT.....CCT CCA G A D P P	GTAAGCTGCA	5	4.0
6	168	431-598	ACCCACACAG	GC ATA.....CTA GTG G G I L V	GTAAGCCATG	6	1.0
7	195	599-793	CCCTATGGAG	GA ATC.....TCC CTG G G I S L	GTAAGCGCCC	7	1.0
8	87	794-880	TATGTTTTAG	GG ATA.....TTG ATA G G I L I	GTAAGGCAAG	8	3.5
9	110	881-990	CTCTCCACAG	CC CAG.....AAG TGG A Q K W	GTACGTTCCT	9	5.0
10	519	991-1509	GTCTCCCCAG	ACC AGA... T R			

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Sequence Variants Identified in Full-Length and Duplicated Genomic Clones

DNA	EXONS CONT.	EXON 6 +/- 497-498			EXON 7 654			EXON 7 690			EXON 10 1269			EXON 10 1335			L76630
CHR15 HYBRID	5-10 1-10		+TG -TG			C/T			G/A		C/C			C/C			6GT 8GT
YAC																	
D-948a10	5-10			-TG			T			A	C			C			6GT
D-853b12	6-10			-TG			T			A	C			C			6GT
D/F 969b11	5-10 1-10		+TG -TG			C/T			G/A			C/T		C/C			6GT 8GT
F-134h10	1-10	+TG			C			G			C			C			8GT
F-776a12	1-10	+TG			C			G			C			C			8GT
F-791e6	1-10	+TG			C			G			C			C			8GT
F-811b6	1-10	+TG			C			G			C			C			8GT
F-953g6	1-10	+TG			C			G			C			C			8GT
F-859c11	1-10	+TG			C			G			C			C			8GT
F-810f11	1-10	+TG			C			G			C			C			8GT
F-801e1	1-10	+TG			C			G			C			C			8GT
BAC																	
F-467o18	1-10	+TG			C			G			C					T	8GT

FIG. 2

DNA	Control #	EXON 6 +/- 497-498			EXON 7 654			EXON 7 690			EXON 10 1269			EXON 10 1335		
Control Genomic DNA	43	+/+ 10	+/- 33	-/- 0	C/C 5	C/T 38	T/T 0	G/G 0	G/A 43	A/A 0	C/C 6	C/T 36	T/T 1	C/C 24	C/T 19	T/T 0

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Expression Analysis of Sequence Variants

	Bases 497-498			Base 654			Base 690			Base 933			Base 1296			Base 1335		
Subj	DNA	1-10 cDNA	5-10 cDNA	DNA	1-10 cDNA	5-10 cDNA	DNA	1-10 cDNA	5-10 cDNA	DNA	1-10 cDNA	5-10 cDNA	DNA	1-10 cDNA	5-10 cDNA	DNA	1-10 cDNA	5-10 cDNA
SL061	+/-	+	+/-	CT	C	CT	GA	G	GA	G	G	G	CT	CT	CT	C	C	C
SL084	+	+	+	C	C	C	GA	G	GA	G	G	G	CT	C	CT	C	C	C
SL111	+/-	+	+/-	CT	C	CT	GA	G	GA	G	G	G	CT	CT	CT	CT	CT	CT
SL097	+	+	+	CT	C	CT	GA	G	GA	G	G	G	CT	C	CT	C	C	C
SL089	+	+	+	C	C	C	GA	GA	GA	GA	GA	GA	CT	CT	CT	C	C	C
SHSY	+/-	+	+/-	CT	C	CT	GA	GA	GA	GA	GA	GA	C	C	C	C	C	C

FIG. 3

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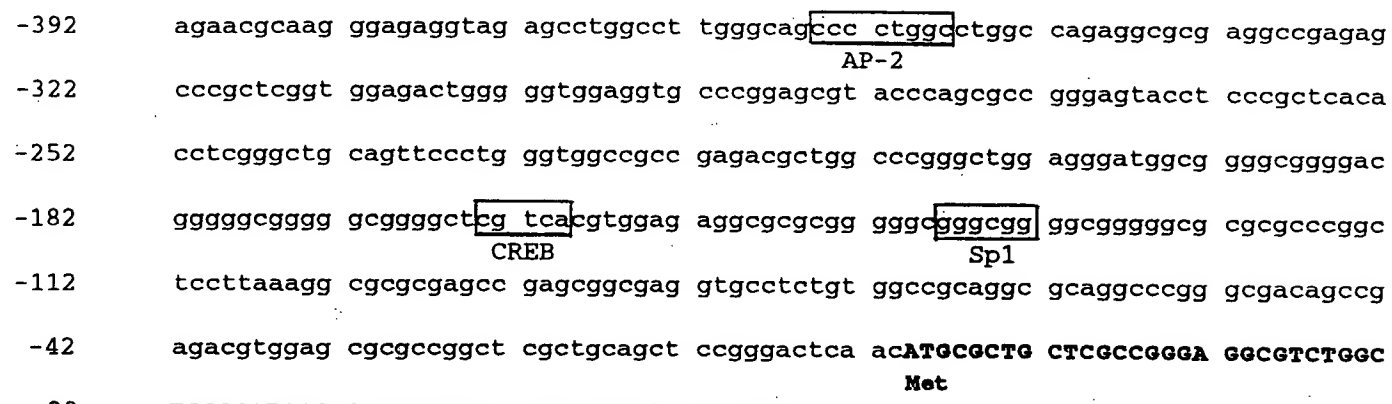

FIG. 4

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PTO

CENTROMERE

TELOMERE

PAC BAC YAC	SIZE kb	D15S942	D15S1043	ALPHA-7 SEQUENCE L76630	EXON10	EXON 9	EXON 8	EXON 7	EXON 6	EXON 5	D15S165	D15S1031	ALPHA-7 SEQUENCE L76630	EXON10	EXON 9	EXON 8	EXON 7	EXON 6	EXON 5	EXON 4	EXON 3	EXON 2	EXON 1	D15S1360	D15S1010	D15S144	D15S1007	D15S995
PAC																												
64a1		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	+	+	+	-	-	-	-
25919		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	+	+	+	-	-	-	-
BAC																												
467o18		-	-	-	-	-	-	-	-	-	-	-	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-
YAC																												
948a10	1730	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
853b12	790	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
895f6	1580	-	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
969b11	1030	-	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-
776a12	1640	-	-	-	-	-	-	-	-	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-
791e6	1170	-	-	-	-	-	-	-	-	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-
811b6	1060	-	-	-	-	-	-	-	-	-	-	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-
953g6	1720	-	-	-	-	-	-	-	-	-	-	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-
134h10	N.A.	-	-	-	-	-	-	-	-	-	-	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-
859c11	1330	-	-	-	-	-	-	-	-	-	-	-	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-
810f11	940	-	-	-	-	-	-	-	-	-	-	-	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-
801e1	1630	-	-	-	-	-	-	-	-	-	-	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
966a4	1500	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	+	-	-
764f8	740	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	+	+
822g2	1280	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	+	+

FIG. 5

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```
                1
EXON D          CAGGCCGCCA  CATAGCTCCC  GCCAAGTCCT  CGGTGCCCCT  TGCCATTTTC  CAGCCGCGTC  CCACGAGGGT
297bp           CACGGCGGCG  GGGAGAGGTG  GAGCCGCGAG  AGCTCGGCCG  GGGGCCCCGC  CTGGTGGCCG  CGGCCATGAC
                AGCGGCTCGG  GACTGGCTCC  TTTTCCGCGC  CCCTCCCGCC  GGAGGTGAGG  GGAAGATGTC  CATGTCAGGG
                TTCAAGGCCA  AACCGAAGTT  ACTGGCCTCT  ATCTTCCAGG  AGAACCAGGA  GCCACAGCCG  CGGCTCACGC
                CCCACCGCAA  CATTAAGgtg  agtcgcc.....
                                297
                                  298
EXON C             ....ctc  atttcagATT  ACAAGTGGAC  ACCTGAGTCA  GCAGGACCTG  GAATCCCAGA  TGAGAGAGCT
125bp           TATCTACACG  ACTCAGATCT  TGTTGTCACC  CCCATTATTG  ACAATCCAAA  GGTGCAGAAA  GCACTCTGAC
                AAgtgagttg  ta.....
                422
                              423
EXON B          ..ttaaccac  agATAATGAA  ACAACCACCA  TCGGTTAAAT  TTGATGCAAA  AATATTGCAT  CTACCAGCAT
64bp            TTTCAGgtag  gatcat.....
                   486
                                487
EXON A           .....ttta  ttctagTTCC  AATTGCTAAT  CCAGCATTTG  TGGATAGCTG  CAAACTGCGA  TATgtaagta
47bp              aca.......                                                          533

                              534
EXON 5          ...ctgtttc  tagTGCTGAT  GAGCGCTTTG  ACGCCACATT  CCACACTAAC  GTGTTGGTGA  ATTCTTCTGG
80bp                        GCATTGCCAG  TACCTGCCTC  CAGgtaagctgca......
                                                    613
                              614
EXON 6          ....acccaca  cagGCATATT  CAAGAGTTCC  TGCTACATCG
27bp                                                      640
```

FIG. 6

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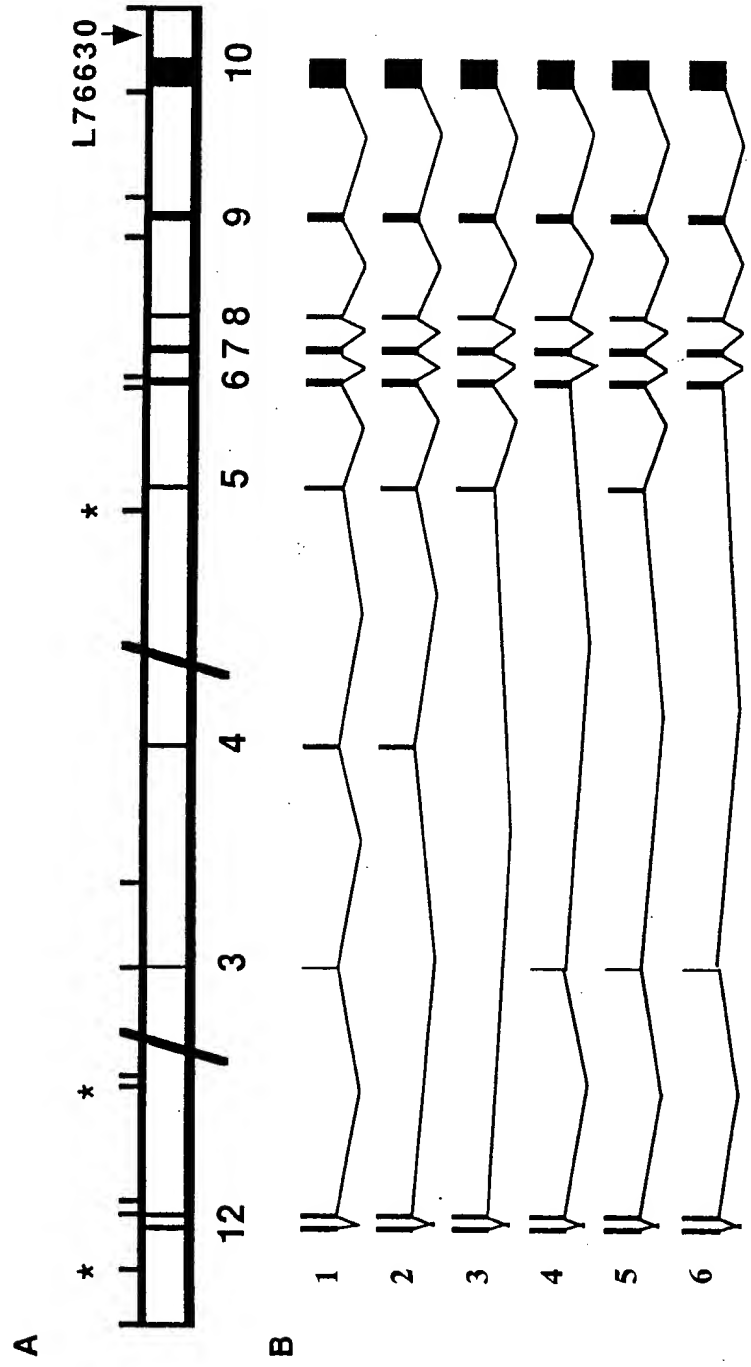

FIG. 7

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```
  1 agaacgcaag ggagaggtag agcctggcct tgggcagccc ctggcctggc cagaggcgcg
 61 aggccgagag cccgctcggt ggagactggg ggtggaggtg cccggagcgt acccagcgcc
121 gggagtacct cccgctcaca cctcgggctg cagttccctg ggtggccgcc gagacgctgg
181 cccgggctgg agggatggcg gggcggggac gggggcgggg gcggggctcg tcacgtggag
241 aggcgcgcgg gggcgggcgg ggcgggggcg cgcgcccggc tccttaaagg cgcgcgagcc
301 gagcggcgag gtgcctctgt ggccgcaggc gcaggcccgg gcgacagccg agacgtggag
361 cgcgccggct cgctgcagct ccgggactca ac
```

FIG. 8

```
  1 caggccgcca catagctccc gccaagtcct cggtgcccct tgccattttc cagccgcgct
 61 cccacgaggg tcacggcggc ggggagaggt ggagccgcga gagctcggcc gggggccccg
121 cctggtggcc gcggccatga cagcggctcg ggactggctc cttttccgcg cccctcccgc
181 cggaggtgag gggaagatgt ccatgtcagg gttcaaggcc aaaccgaagt tactggcctc
241 tatcttccag gagaaccagg agccacagcc gcggctcacg ccccaccgca acattaagat
301 tacaagtgga cacctgagtc agcaggacct ggaatcccag atgagagagc ttatctacac
361 gactcagatc ttgttgtcac ccccattatt gacaatccaa aggtgcagaa agcactctga
421 caaataatga aacaaccacc atcggttaaa tttgatgcaa aaatattgca tctaccagca
481 ttttcagttc caattgctaa tccagcattt gtggatagct gcaaactgcg atattgctga
541 tgagcgcttt gacgccacat tccacactaa cgtgttggtg aattcttctg ggcattgcca
601 gtacctgcct ccaggcatat tcaagagttc ctgctacatc g
```

FIG. 9

```
  1 agccctttcc caggcggtag cgggggcagt ggtgctgttg ccctttttaaa ctgcggcttg
 61 acgggagccg cgcctcctgt cggtggagtc ggttataaag ggagcagccc cgcaggccgc
121 cacatagctc ccgccaagtc ctcggtgccc cttgccattt tccagccgcg ctcccacgag
181 ggtcacggcg gcggggagag gtggagccgc gagagctcgg ccgggggccc cgcctggtgg
241 ccgcggccat gacagcggct cgggactggc tccttttccg cgcccctccc gccggaggtg
301 aggggaagat gtccatgtca gggttcaagg ccaaaccgaa gttactggcc tctatcttcc
361 aggagaacca ggagccacag ccgcggctca cgccccaccg caacattaag attacaagtg
421 gacacctgag tcagcaggac ctggaatccc agatgagaga gcttatctac acgactcaga
481 tcttgttgtc acccccatta ttgacaatcc aaaggtgcag aaagcactct gacaattcca
541 attgctaatc cagcatttgt ggatagctgc aaactgcgat attgctgatg agcgctttga
601 cgccacattc cacactaacg tgttggtgaa ttcttctggg cattgccagt acctgcctcc
661 aggcatattc aagagttcct gctacatcg
```

FIG. 10